



SEQUENCE LISTING

<110> François, Cedric

<120> COMPOSITIONS AND METHODS FOR TREATING TRANSPLANTS

<130> 09799910-0042

<140> 10/724526

<141> 2003-11-28

<160> 8

<170> PatentIn version 3.2

<210> 1

<211> 399

<212> DNA

<213> Artificial sequence

<220>

<223> artificial gene for streptavidin

<400> 1

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acgctgaaag ccgttatggt ctgaccggtc gttacgactc tgctccggct accgacgggt 180

ctgggtactgc tctgggttg accgttgctt ggaaaaacaa ctaccgtaac gctcactctg 240

ctaccacctg gtctggccag tacgttggtg gtgctgaagc tcgtatcaac acccagtggc 300

tgctgacctc tggtagcacc gaagctaacg cttggaaatc taccctggtt ggtagcagaca 360

cgttcaccaa agttaaacg tctgctgctt ctatctaga 399

<210> 2

<211> 128

<212> PRT

<213> Artificial sequence

<220>

<223> polypeptide sequence of artificial gene for streptavidin (encoded
by SEQ ID NO:1)

<400> 2

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Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr Tyr
20 25 30

Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly Arg
 35 40 45

Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly Trp
 50 55 60

Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser Ala Thr Thr
 65 70 75 80

Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile Asn Thr Gln
 85 90 95

Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser Thr
 100 105 110

Leu Val Gly His Asp Thr Phe Thr Lys Val Lys Pro Ser Ala Ala Ser
 115 120 125

<210> 3
 <211> 604
 <212> DNA
 <213> Gallus gallus

<400> 3
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 aaagtgctcg ctgactggga aatggaccaa cgatctgggc tccaacatga ccatcggggc 180
 tgtgaacagc agaggtgaat tcacaggcac ctacatcaca gccgtaacag ccacatcaaa 240
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 cacctttggc ttcaccgtca attggaagtt ttcagagtcc accactgtct tcacgggcca 360
 gtgcttcata gacaggaatg ggaaggaggt cctgaagacc atgtggctgc tgcgggtcaag 420
 tgттаатгac attggtgatg actggaaagc taccagggtc ggcatcaaca tcttcaactg 480
 cctgcgcaca cagaaggagt gaggatggcc ccgcaaagcc agcaacaatg ccggagtgtc 540
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 attc 604

<210> 4
 <211> 152
 <212> PRT

<213> Gallus gallus

<400> 4

Met Val His Ala Thr Ser Pro Leu Leu Leu Leu Leu Leu Ser Leu
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Ala Leu Val Ala Pro Gly Leu Ser Ala Arg Lys Cys Ser Leu Thr Gly
20 25 30

Lys Trp Thr Asn Asp Leu Gly Ser Asn Met Thr Ile Gly Ala Val Asn
35 40 45

Ser Arg Gly Glu Phe Thr Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr
50 55 60

Ser Asn Glu Ile Lys Glu Ser Pro Leu His Gly Thr Gln Asn Thr Ile
65 70 75 80

Asn Lys Arg Thr Gln Pro Thr Phe Gly Phe Thr Val Asn Trp Lys Phe
85 90 95

Ser Glu Ser Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp Arg Asn
100 105 110

Gly Lys Glu Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser Val Asn
115 120 125

Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn Ile Phe
130 135 140

Thr Arg Leu Arg Thr Gln Lys Glu
145 150

<210> 5

<211> 399

<212> DNA

<213> Rattus norvegicus

<400> 5

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acgctgaaag ccgttatgtt ctgaccgggtc gttacgactc tgctccggct accgacgggt 180

ctgggtactgc tctgggttg accgttgctt ggaaaaacaa ctaccgtaac gctcactctg 240

ctaccacctg gtctggccag tacgttggtg gtgctgaagc tcgtatcaac acccagtggc 300
 tgctgacctc tggtagacc gaagctaacg cttggaaatc taccctgggtt ggtagcagaca 360
 cgttcaccaa agttaaacg tctgctgctt ctatctaga 399

<210> 6
 <211> 278
 <212> PRT
 <213> Rattus norvegicus

<400> 6

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 20 25 30

Pro Ser Ser Gly Pro Arg Gly Pro Gly Gln Arg Arg Pro Pro Pro Pro
 35 40 45

Pro Pro Pro Pro Ser Pro Leu Pro Pro Pro Ser Gln Pro Pro Pro Leu
 50 55 60

Pro Pro Leu Ser Pro Leu Lys Lys Lys Asp Asn Ile Glu Leu Trp Leu
 65 70 75 80

Pro Val Ile Phe Phe Met Val Leu Val Ala Leu Val Gly Met Gly Leu
 85 90 95

Gly Met Tyr Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu Arg
 100 105 110

Glu Phe Thr Asn His Ser Leu Arg Val Ser Ser Phe Glu Lys Gln Ile
 115 120 125

Ala Asn Pro Ser Thr Pro Ser Glu Thr Lys Lys Pro Arg Ser Val Ala
 130 135 140

His Leu Thr Gly Asn Pro Arg Ser Arg Ser Ile Pro Leu Glu Trp Glu
 145 150 155 160

Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys Gly
 165 170 175

Gly Leu Val Ile Asn Glu Ala Gly Leu Tyr Phe Val Tyr Ser Lys Val
180 185 190

Tyr Phe Arg Gly Gln Ser Cys Asn Ser Gln Pro Leu Ser His Lys Val
195 200 205

Tyr Met Arg Asn Phe Lys Tyr Pro Gly Asp Leu Val Leu Met Glu Glu
210 215 220

Lys Lys Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser Ser
225 230 235 240

Tyr Leu Gly Ala Val Phe Asn Leu Thr Val Ala Asp His Leu Tyr Val
245 250 255

Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr Phe
260 265 270

Phe Gly Leu Tyr Lys Leu
275

<210> 7
<211> 972
<212> DNA
<213> Homo sapiens

<400> 7
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cagctctccc tgggcccctc caggcacagt tcttccctgt ccaacctctg tgcccagaag 180
gcctggtcaa aggaggccac caccaccacc gccaccgcca ccactaccac ctccgccgcc 240
gccgccacca ctgcctccac taccgctgcc acccctgaag aagagaggga accacagcac 300
aggcctgtgt ctcttgtga tgtttttcat ggttctggtt gccttggtag gattgggcct 360
ggggatgttt cagctcttcc acctacagaa ggagctggca gaactccgag agtctaccag 420
ccagatgcac acagcatcat ctttgagaa gcaaataaggc caccacagtc caccctga 480
aaaaaggag ctgaggaaa tggccattt aacaggcaag tccaactcaa ggtccatgcc 540
tctggaatgg gaagacacct atggaattgt cctgctttct ggagtgaagt ataagaagg 600
tggccttggtg atcaatgaaa ctgggctgta cttgtatat tccaaagtat acttccgggg 660

tcaatcttgc aacaacctgc ccctgagcca caaggtctac atgaggaact ctaagtatcc	720
ccaggatctg gtgatgatgg aggggaagat gatgagctac tgcactactg ggcagatgtg	780
ggcccgagc agctacctgg gggcagtgtt caatcttacc agtgctgac atttatatgt	840
caacgtatct gagctctctc tgggtcaattt tgaggaatct cagacgtttt tcggcttata	900
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<210> 8
 <211> 281
 <212> PRT
 <213> Homo sapiens

<400> 8

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Ser	Ser	Ala	Ser	Ser	Pro	Trp	Ala	Pro	Pro	Gly	Thr	Val	Leu	Pro	Cys
			20					25					30		

Pro	Thr	Ser	Val	Pro	Arg	Arg	Pro	Gly	Gln	Arg	Arg	Pro	Pro	Pro	Pro
		35					40					45			

Pro	Pro	Pro	Pro	Pro	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro
	50					55				60					

Pro	Leu	Pro	Leu	Pro	Pro	Leu	Lys	Lys	Arg	Gly	Asn	His	Ser	Thr	Gly
65						70				75					80

Leu	Cys	Leu	Leu	Val	Met	Phe	Phe	Met	Val	Leu	Val	Ala	Leu	Val	Gly
				85					90					95	

Leu	Gly	Leu	Gly	Met	Phe	Gln	Leu	Phe	His	Leu	Gln	Lys	Glu	Leu	Ala
			100					105					110		

Glu	Leu	Arg	Glu	Ser	Thr	Ser	Gln	Met	His	Thr	Ala	Ser	Ser	Leu	Glu
		115					120					125			

Lys	Gln	Ile	Gly	His	Pro	Ser	Pro	Pro	Pro	Glu	Lys	Lys	Glu	Leu	Arg
	130					135					140				

Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu
 145 150 155 160

Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr
 165 170 175

Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
 180 185 190

Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser
 195 200 205

His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met
 210 215 220

Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala
 225 230 235 240

Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His
 245 250 255

Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser
 260 265 270

Gln Thr Phe Phe Gly Leu Tyr Lys Leu
 275 280